



**Figure S1** Rarefaction data from Illumina sequencing experiments. Reads from each water and mosquito library were sampled starting at 100 sequences per step and increased in increments of 50 until the total number of reads per sample was reached. Each step was sampled 10 times. Each line represents the smoothed mean across each increment for OTUs clustered at a sequence similarity threshold of 97%. Lines for each larval and water sample across all field and laboratory sites and sampling dates are shown. Each site and sampling date is shown with a different color while each species or water sample is indicated by different line fonts as shown in the legend.